

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.
- (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND
USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sheridan Ross P.C.
 - (B) STREET: 1700 Lincoln St., Suite 3500
 - (C) CITY: Denver
 - (D) STATE: Colorado
 - (E) COUNTRY: USA
 - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,666
 - (B) FILING DATE: 04-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,941
 - (B) FILING DATE: 04-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Crook, Wannell M.
 - (B) REGISTRATION NUMBER: 31,071
 - (C) REFERENCE/DOCKET NUMBER: 3553-18
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (303) 863-9700
 - (B) TELEFAX: (303) 863-0223

Thr"

- (xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
20 25

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(ix) FEATURE:
      (A) NAME/KEY: Region
      (B) LOCATION: 16
      (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
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(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa
1           5           10           15

Val Glu Val Xaa
                20

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA      48
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
1           5           10           15

CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG      96
Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
                20           25           30

CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT      144
Leu Tyr Arg Gln Pro Asp Gly Val Ala Ala Leu Leu Asp Ile Cys
                35           40           45

CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT      192
Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
                50           55           60

CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGC CAG TGC      240
Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
        65           70           75           80

GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC      288
Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
                85           90           95

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CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro 100 105 110	336
GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys 115 120 125	384
CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp 130 135 140	432
TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala 145 150 155 160	480
CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu 165 170 175	528
GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys 180 185 190	576
ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CGC GGC Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly 195 200 205	624
GCC AAT ACC CCC GTC GAC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val 210 215 220	672
AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys 225 230 235 240	720
GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr 245 250 255	768
GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile 260 265 270	816
GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala 275 280 285	864
CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 290 295 300	912
GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp 305 310 315 320	960

GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC 1008
 Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
 325 330 335

GAA GCC GCC TGA 1020
 Glu Ala Ala *
 340

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
 1 5 10 15
 Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
 20 25 30
 Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
 35 40 45
 Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
 50 55 60
 Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
 65 70 75 80
 Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
 85 90 95
 Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
 100 105 110
 Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys
 115 120 125
 Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp
 130 135 140
 Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala
 145 150 155 160
 Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu
 165 170 175
 Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys
 180 185 190

Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
 195 200 205
 Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
 210 215 220
 Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
 225 230 235 240
 Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
 245 250 255
 Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
 260 265 270
 Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
 275 280 285
 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
 290 295 300
 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
 305 310 315 320
 Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
 325 330 335
 Glu Ala Ala *
 340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG ACC TAT GTC GTC ACC GAC GCC TGC ATC AAG TGC AAG TAC ATG GAC	48
Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp	
1 5 10 15	
TGC GTG GAA GTC TGC CCT GTG GAC TGC TTC TAC GAA GGC GAG AAC ATG	96
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met	
20 25 30	

CTC GTC ATC AAT CCC AGT GAA TGC ATC GAC TGC GGC GTC TGC GAA CCG 144
 Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro
 35 40 45

GAA TGC CCA GCC GAA GCC ATC CTT CCC GAC ACC GAA AGC GGT CTC GAG 192
 Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu
 50 55 60

CAG TGG ATG GAA CTG AAC ACG AAG TAC TCG GCC GAG TGG CCG AAT CTC 240
 Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu
 65 70 75 80

ACG TCC AAG AAA GAT TCG CCG GAA GAT GCC GAC GAG TAC AAG GGC GTG 288
 Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val
 85 90 95

GAA GGC AAG TTC GAG AAG TTC TTC TCG CCC GAG CCC GGC GAG GGC GAC 336
 Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp
 100 105 110

TGA 339
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp
 1 5 10 15

Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met
 20 25 30

Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro
 35 40 45

Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu
 50 55 60

Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu
 65 70 75 80

Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val
 85 90 95

Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp
 100 105 110

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